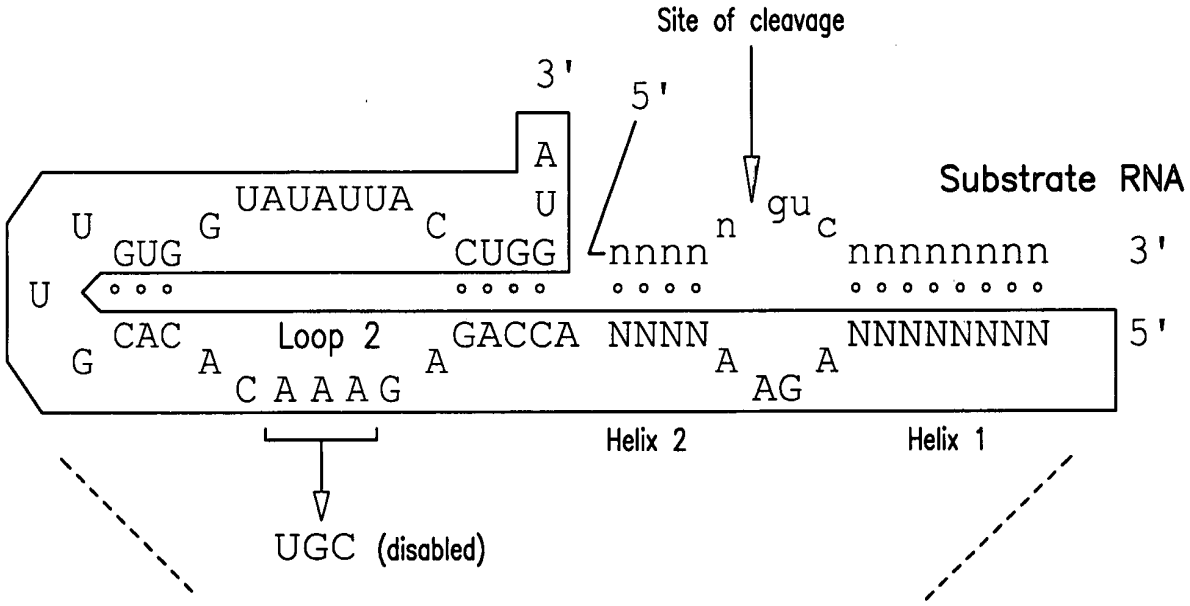

FIG. 1A

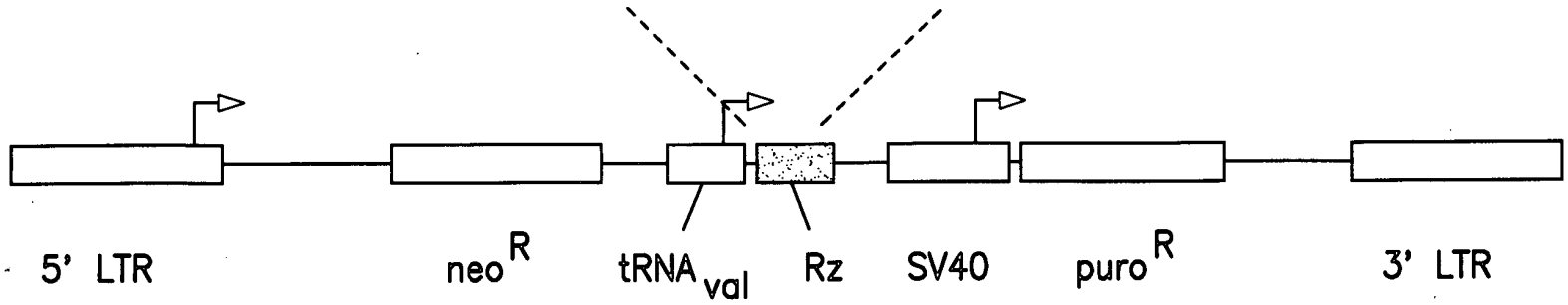

FIG. 1B

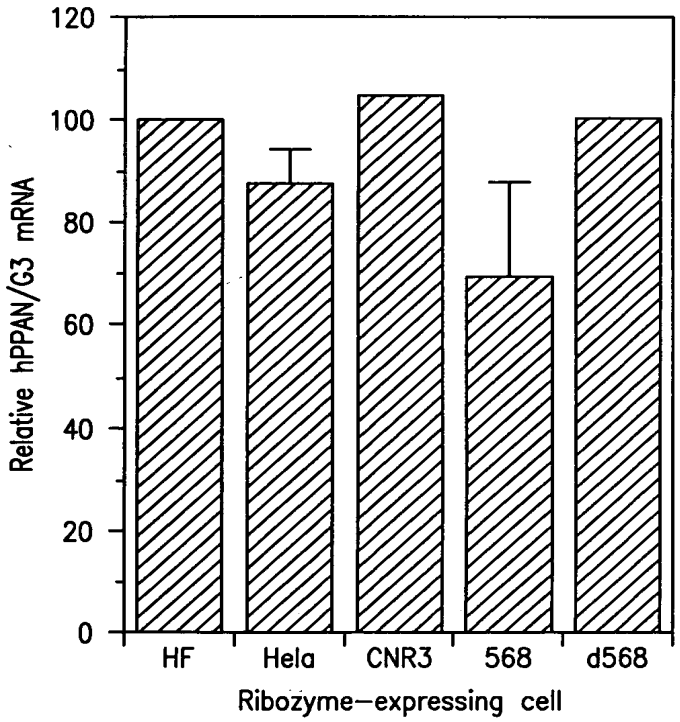

FIG. 3A

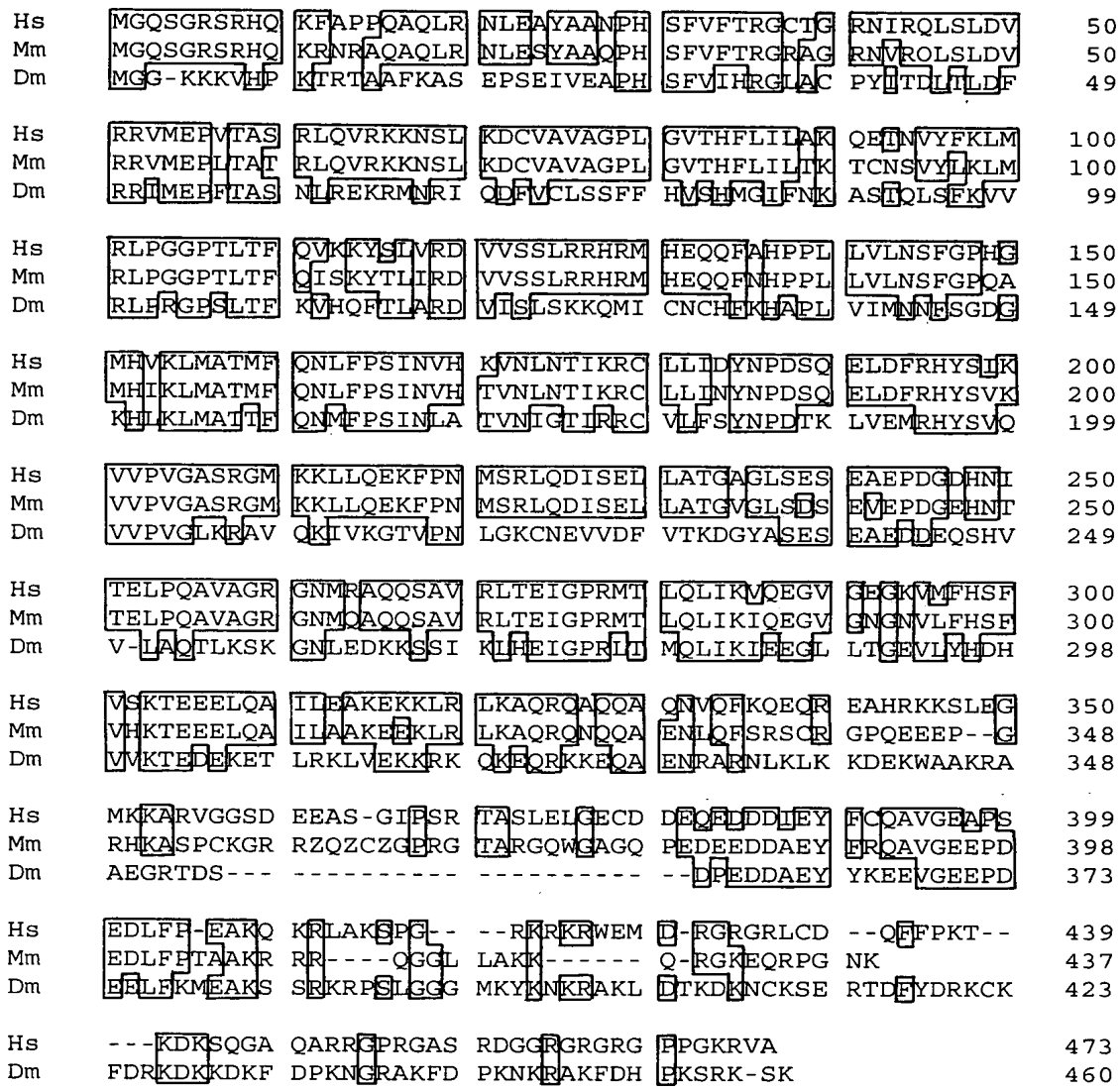

FIG. 3B

```
      |   10      |   20      |   30      |   40      |   50      |   60
    1 GCCTGATGTC GTCCCACGCC GTGCCGGCTC TCAGGCGCCG GAAGTGAGCT GCGCACGGCC   60
   61 GGAAGCGGCG GACGCAGGAG GCCTCGTGGA GGACACAGCA GCATGGGACA GTCAGGGAGG  120
  121 TCCCGGCACC AGAAGCGCGC CCCGCCCCAG GCGCAGCTCC GCAACCTCGA GGCCTATGCC  180
  181 GCGAACCCGC ACTCGTTCGT GTTCACGCGA GGCTGCACGG GTCGCAACAT CCGGCAGCTC  240
  241 AGCCTGGACG TGCGGCGGGT CATGGAGCCC GTCACTGCCA GCCGTCTGCA GGTTCGTAAG  300
  301 AAGAACTCGC TGAAGGACTG CGTGGCAGTG GCTGGGCCCC TCGGGGTCAC ACACTTTCTG  360
  361 ATCCTAGCAA AACAAGAGAC CAATGTCTAC TTTAAGCTGA TGCGCCTCCC AGGAGGCCCC  420
  421 ACCTTGACCT TCCAGGTCAA GAAGTACTCG CTGGTGCGTG ATGTGGTCTC CTCACTGCGC  480
  481 CGGCACCGCA TGCACGAGCA GCAGTTTGCC CACCCACCCC TCCTGGTACT CAACAGCTTT  540
  541 GGCCCCCATG GTATGCATGT GAAGCTCATG GCCACCATGT TCCAGAACCT GTTCCCCTCC  600
  601 ATCAACGTGC ACAAGGTGAA CCTGAACACC ATCAAGCGCT GCCTCCTCAT CGACTACAAC  660
  661 CCCGACTCCC AGGAGCTGGA CTTCCGCCAC TATAGCATCA AAGTTGTTCC TGTGGGCGCG  720
  721 AGTCGCGGGA TGAAGAAGCT GCTCCAGGAG AAGTTCCCCA ACATGAGCCG CCTGCAGGAC  780
  781 ATCAGCGAGC TGCTGGCCAC GGGCGCGGGG CTGTCGGAGA GCGAGGCAGA GCCTGACGGC  840
  841 GACCACAACA TCACAGAGCT GCCTCAGGCT GTCGCTGGCC GTGGCAACAT GCGGGCCCAG  900
  901 CAGAGTGCAG TGCGGCTCAC CGAGATCGGC CCGCGGATGA CACTGCAGCT CATCAAGGTC  960
  961 CAGGAGGGCG TCGGGGAGGG CAAAGTGATG TTCCACAGTT TTGTGAGCAA GACGGAGGAG 1020
 1021 GAGCTGCAGG CCATCCTGGA AGCCAAGGAG AAGAAGCTGC GGCTGAAGGC TCAGAGGCAG 1080
 1081 GCCCAGCAGG CCCAGAATGT GCAGCGCAAG CAGGAGCAGC GGGAGGCCCA CAGAAAGAAG 1140
 1141 AGCCTGGAGG GCATGAAGAA GGCACGGGTC GGGGGTAGTG ATGAAGAGGC CTCTGGGATC 1200
 1201 CCTTCAAGGA CGGCGAGCCT GGAGTTGGGT GAGGACGATG ATGAACAGGA AGATGATGAC 1260
 1261 ATCGAGTATT TCTGCCAGGC GGTGGGCGAG GCGCCCAGTG AGGACCTGTT CCCCGAGGCC 1320
 1321 AAGCAGAAAC GGCTTGCCAA GTCTCCAGGG CGGAAGCGGA AGCGGTGGGA AATGGATCGA 1380
 1381 GGCAGGGGTC GCCTTTGTGA CCAGAAGTTT CCCAAGACCA AGGACAAGTC CCAGGGAGCC 1440
 1441 CAGGCCAGGC GGGGGCCCAG AGGGGCTTCC CGGGATGGTG GGCGAGGCCG GGGCCGAGGC 1500
 1501 CGCCCAGGGA AGAGAGTGGC CTGAGCCCAA GCCGCACCGG AGCAGCGGCT GGATTGAACG 1560
 1561 CCCCAGATTG GGGCCCGAGA TGTGGCCCTC GGTTTCCTTT CATAAAGGAG TTGTGTCCCC 1620
 1621 AGCCCTTCCA CTCCAGTAAA GAACTGAATT GGCAAAAAAA AAAA                   1664
      |   10      |   20      |   30      |   40      |   50      |   60
```

FIG. 6A

```
      |   10      |   20      |   30      |   40      |   50      |   60
    1 MGQSGRSRHQ KRAPPQAQLR NLEAYAANPH SFVFTRGCTG RNIRQLSLDV RRVMEPVTAS   60
   61 RLQVRKKNSL KDCVAVAGPL GVTHFLILAK QETNVYFKLM RLPGGPTLTF QVKKYSLVRD  120
  121 VVSSLRRHRM HEQQFAHPPL LVLNSFGPHG MHVKLMATMF QNLFPSINVH KVNLNTIKRC  180
  181 LLIDYNPDSQ ELDFRHYSIK VVPVGASRGM KKLLQEKFPN MSRLQDISEL LATGAGLSES  240
  241 EAEPDGDHNI TELPQAVAGR GNMRAQQSAV RLTEIGPRMT LQLIKVQEGV GEGKVMFHSF  300
  301 VSKTEEELQA ILEAKEKKLR LKAQRQAQQA QNVQRKQEQR EAHRKKSLEG MKKARVGGSD  360
  361 EEASGIPSRT ASLELGEDDD EQEDDDIEYF CQAVGEAPSE DLFPEAKQKR LAKSPGRKRK  420
  421 RWEMDRGRGR LCDQKFPKTK DKSQGAQARR GPRGASRDGG RGRGRGRPGK RVAZ        474
      |   10      |   20      |   30      |   40      |   50      |   60
```

FIG. 6B

```
MM                                FGQGGKQAAWGSPGGPDIRSAIAPGELRNLESYAAQPHSFV  41
HS

MM      FTRG---RAGRNVRQLSLDVRRVMEPLTATRLQVRKKNSLKDCVAVAGPLGVTHFLITLTK  98
HS                                                    LGPRVTHFLITLSK  13

MM      TD--NSVYLKLMRLEGGHTLTFQISKYTLIRDVVSSLRRH-RMHEQQFNHPPLLVLNSFG  155
HS      TE--TNVYFKLMRLEGGHTLTFQVKKYSLVRDVVSSLRRH-RMHEQQFAHPPLLVLNSFG  70

MM      PQG---------MHIKLMATMFQNLFPSINVHTVNLNTIKRQLLINYNPD-SQELDFRHY  205
HS      PHG---------MHVKLMATMFQNLFPSINVHKVNLNTIKRQSSXDLKEGFPRSLDFRPI  121

MM      SVKVVPVGASRGMKKLLQ------EKFPNMSRLQDISELLATGVG---------------  244
HS      IAFKGGSCWAPNSGGL                                              137

MM      --------------------LSDSEVEPDGEHN------TTELPQAVAG-RGNMQAQQSA  277

MM      VRLIEIGPRMILQLIKIQEGVGNGNVLFHSFVHKTEEELQAILAAKEEKLRLKAQRQNQQ  337

MM      AENLQRXRSCRXPTRRRAWQA-------------------------------------  358
```

FIG. 7